

L Number	Hits	Search Text	DB	Time stamp
1	2	5955309.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:04
2	2	5874243.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:05
3	2	6043054.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:05
4	2	5976834.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
5	2	5955308.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
6	2	6048711.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:06
-	2	6262246.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/08/31 11:04
-	13	gerald-christophe-p-g.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:40
-	38	jones-kenneth-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:40
-	19	bonini-james-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41
-	16	borowsky-beth.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41
-	13	npff adj receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/10/01 12:41

## 09866248 Results

SEQ ID NO: 6

Result No.	Score	Query Match	Length	DB	ID	Description
1	2208	100.0	420	2	AAW81358	Aaw81358 Human 7-t
2	2208	100.0	420	3	AAV79375	Aay79375 Human neu
3	2208	100.0	420	3	AAV99930	Aay99930 HLWAR77 p
4	2208	100.0	420	4	AAU00233	Aau00233 Orphan re
5	2208	100.0	420	5	AAU79013	Aau79013 Human G p
6	2208	100.0	522	4	ABB11723	Abb11723 Human GPC
7	2208	100.0	522	7	ADC89684	Adc89684 Human neu
8	2204	99.8	420	3	AAB07426	Aab07426 Amino aci
9	2204	99.8	522	4	AAU00234	Aau00234 Orphan re
10	2204	99.8	522	6	ABG73522	Abg73522 Human G-p
11	2204	99.8	522	6	ABP82012	Abp82012 Human neu
12	2115	95.8	408	3	AAV76882	Aay76882 Human NPY
13	1730.5	78.4	417	3	AAV79377	Aay79377 Rat neuro
14	1719	77.9	332	4	AAU18133	Aau18133 Novel hum
15	1719	77.9	332	4	AAU18688	Aau18688 Renal and
16	1719	77.9	332	4	AAU21718	Aau21718 Novel hum

Result No.	Score	Query Match	Length	DB	ID	Description
1	2208	100.0	420	3	US-09-255-368-6	Sequence 6, Appli
2	1060	48.0	430	3	US-09-255-368-8	Sequence 8, Appli
3	1024	46.4	432	3	US-09-255-368-2	Sequence 2, Appli
4	525.5	23.8	444	3	US-09-119-788-2	Sequence 2, Appli
5	525.5	23.8	444	4	US-09-426-290-2	Sequence 2, Appli
6	499.5	22.6	402	3	US-08-846-704-4	Sequence 4, Appli
7	499.5	22.6	402	4	US-08-462-509B-2	Sequence 2, Appli
8	499.5	22.6	402	5	PCT-US95-05616-2	Sequence 2, Appli
9	499.5	22.6	425	3	US-08-846-704-2	Sequence 2, Appli
10	499.5	22.6	425	4	US-09-479-128-2	Sequence 2, Appli
11	499.5	22.6	425	4	US-09-211-823C-22	Sequence 22, Appl
12	476.5	21.6	369	4	US-08-462-509B-4	Sequence 4, Appli

## RESULT 1

US-09-255-368-6

; Sequence 6, Application US/09255368

; Patent No. 6262246

; GENERAL INFORMATION:

; APPLICANT: Gerald, Christophe P.G.

; APPLICANT: Jones, Kenneth A.

; APPLICANT: Bonini, James A.

; APPLICANT: Borowsky, Beth

; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

; TITLE OF INVENTION: and Uses Thereof

; FILE REFERENCE: 1795/57155-A

; CURRENT APPLICATION NUMBER: US/09/255,368

; CURRENT FILING DATE: 1999-02-22

; EARLIER APPLICATION NUMBER: 09/161,113

; EARLIER FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.0 - beta

; SEQ ID NO 6

; LENGTH: 420

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-255-368-6

Query Match 100.0%; Score 2208; DB 3; Length 420;

Best Local Similarity 100.0%; Pred. No. 2.4e-200;

Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEKWDTNSSSENWHPIWNVNDTKHHLYS DINITV VNYLHQPQVAAIFIISYFLIFFLCM 60  
|||||

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Db      1 MNEKWDTNSSSENWHPIWNVNDTKHHLYSDINITYVNYLHQPVAAIFIISYFLIFFLCM 60
Qy      61 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIAGWPFNGTMCKI 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIAGWPFNGTMCKI 120
Qy     121 SGLVQGISVAASVFTLVAVDRFQCVVYPFKPKLTIKTAFVIIMIIVWLAITIMSPSAV 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 SGLVQGISVAASVFTLVAVDRFQCVVYPFKPKLTIKTAFVIIMIIVWLAITIMSPSAV 180
Qy     181 MLHVQEEKYYRVRLNSQNKTSPVYWCREDPNQEMRKIYTTVLFANIYLAFLSLIVIMYG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 MLHVQEEKYYRVRLNSQNKTSPVYWCREDPNQEMRKIYTTVLFANIYLAFLSLIVIMYG 240
Qy     241 RIGISLFRAAVPHTGRKNQEQWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMLSDYA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 RIGISLFRAAVPHTGRKNQEQWHVVSRRKKQKIIKMLLIVALLFILSWLPLWTLMLSDYA 300
Qy     301 DLSPNELQIINIYIYPFAHWLAFGNSSVNPPIYGFNENFRRGFQEAFLQLCQKRAKPM 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 DLSPNELQIINIYIYPFAHWLAFGNSSVNPPIYGFNENFRRGFQEAFLQLCQKRAKPM 360
Qy     361 EAYALKAKSHVLINTSNQLVQESTFQNPHGFTLLYRKSAEKPQQLVMEELKETTSSEI 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 EAYALKAKSHVLINTSNQLVQESTFQNPHGFTLLYRKSAEKPQQLVMEELKETTSSEI

```

# SUMMARIES

Query						
Result No.	Score	Match	Length	DB	ID	Description
1	485.5	22.0	449	2	A41738	neuropeptide Y rec
2	480	21.7	423	2	B40470	glucocorticoid-ind
3	465	21.1	381	2	I39187	neuropeptide Y/pep
4	460	20.8	443	2	D40470	glucocorticoid-ind
5	445.5	20.2	444	2	A42685	cholecystokinin re
6	444.5	20.1	384	2	A45490	neuropeptide Y/pep
7	444	20.1	382	2	B46133	neuropeptide Y/pep
8	443.5	20.1	349	2	S12863	G protein-coupled
9	443	20.1	428	2	JN0692	cholecystokinin ty
10	437	19.8	382	2	S27388	neuropeptide Y rec
11	437	19.8	491	2	C40470	glucocorticoid-ind
12	436	19.7	436	2	JC5599	cholecystokinin-A
13	435	19.7	370	1	I52315	G protein-coupled

## RESULT 1

A41738

neuropeptide Y receptor - fruit fly (Drosophila melanogaster)

N;Alternate names: G protein-coupled receptor PR4

C;Species: Drosophila melanogaster

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 20-Apr-2000

C;Accession: A41738

R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992

A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from Drosophila melanogaster.

A;Reference number: A41738; MUID:92112730; PMID:1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIA>

A;Cross-references: GB:M81490; NID:g157996; PIDN:AAA28727.1; PID:g157997

C;Genetics:

A;Gene: FlyBase:NepYr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neurokinin 1 receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 22.0%; Score 485.5; DB 2; Length 449;  
Best Local Similarity 34.3%; Pred. No. 1.4e-32;

Matches 107; Conservative 52; Mismatches 114; Indels 39; Gaps 7;

Qy	49	IISYFL---IFFLCMMGNTVVC	FIVMRNKHMTVTNLFILNL	LAISDLLVGIFCMPITLLD	105
			:	:         :	
Db	91	IIVYMLYIPIFIFALIGNGT	VVCYIVYSTPRMRTVTNY	FIASLAIGDILMSFFCEPSS	FIS 150
Qy	106	NIIAG-WPFGNTMCKISGLV	QGISVAASVFTLV	IAVDRFQCVVYPFKPKLTI	KTAFAVII 164
			:	:       :       : :     :	
Db	151	LFILNYWPFGLALCHFVNYS	QAVSVLVSAITLVAISID	RYIAIMWPLKPRITKRYAT	FII 210
Qy	165	MIIWVLAITIMSPSAVM---	LHVQEEKYYRVLNSQNKT	SPVYWCREDPNQEM	215
		:   :	:	:	
Db	211	AGVWFIALATALPIPIVSG	LDPMSPWHTKCEKYI---	CREMWPSRSQ	255
Qy	216	RKIYTTVLFIANIYLAFLS	LIVIMYGRIGISLFRAAV	PHTGRKNQEQWHVVSRRK	QKIIKM 275
			:   :	:     :   :   :	
Db	256	EYYTTLSEFALQFVPLGL	VLIIFTYARITIRVWAKR	PPGEAETNRDQ--RMAR	SKRKMVKM 313
Qy	276	LLIVALLFILSWLPLWTL	MML---SDYADLSPNELQ	IINIYIYPFAHWLAFGN	SSVNPPII 332
		:     :	:	:         :	
Db	314	MLTVVIVFTCCWLFPNQL	LLLNDDEFAHWDPLP---	YVWFAFWLAMSHCCYN	PPII 367
Qy	333	YGFFNENFRRGF	344		
		:			
Db	368	YCYMNARFRSGF	379		

# SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	2208	100.0	522	1	NFF2_HUMAN	Q9y5x5 homo sapien	
2	1730.5	78.4	417	1	NFF2_RAT	Q9eqd2 rattus norv	
3	1060	48.0	430	1	NFF1_HUMAN	Q9gzq6 homo sapien	

## RESULT 1

### NFF2\_HUMAN

ID NFF2\_HUMAN STANDARD; PRT; 522 AA.

AC Q9Y5X5; Q96RV1; Q9NR49;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neuropeptide FF receptor 2 (Neuropeptide G protein-coupled receptor)

DE (G-protein-coupled receptor HLWAR77).

GN GPR74 OR NPGPR OR NPFF2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.

RC TISSUE=Fetal;

RX MEDLINE=99180505; PubMed=10079187;

RA Cikos S., Gregor P., Koppel J.;

RT "Sequence and tissue distribution of a novel G-protein-coupled

RT receptor expressed prominently in human placenta.";

RL Biochem. Biophys. Res. Commun. 256:352-356(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.

RC TISSUE=Brain;

RX MEDLINE=20408933; PubMed=10851242;

RA Elshourbagy N.A., Ames R.S., Fitzgerald L.R., Foley J.J.,

RA Chambers J.K., Szekeres P.G., Evans N.A., Schmidt D.B., Buckley P.T.,

RA Dytko G.M., Murdock P.R., Milligan G., Groarke D.A., Tan K.B.,

RA Shabon U., Nuthulaganti P., Wang D.Y., Wilson S., Bergsma D.J.,

RA Sarau H.M.;

RT "Receptor for the pain modulatory neuropeptides FF and AF is an orphan

RT G protein-coupled receptor.";

RL J. Biol. Chem. 275:25965-25971(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.  
 RC TISSUE=Spinal cord;  
 RX MEDLINE=20564301; PubMed=11024015;  
 RA Bonini J.A., Jones K.A., Adham N., Forray C., Artymyshyn R.,  
 RA Durkin M.M., Smith K.E., Tamm J.A., Boteju L.W., Lakhani P.P.,  
 RA Raddatz R., Yao W.-J., Ogozalek K.L., Boyle N., Kouranova E.V.,  
 RA Quan Y., Vaysse P.J., Wetzel J.M., Branchek T.A., Gerald C.,  
 RA Borowsky B.;  
 RT "Identification and characterization of two G protein-coupled  
 RT receptors for neuropeptide FF.";  
 RL J. Biol. Chem. 275:39324-39331(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RX MEDLINE=20299143; PubMed=10837915;  
 RA Parker R.M.C., Copeland N.G., Eyre H.J., Liu M., Gilbert D.J.,  
 RA Crawford J., Couzens M., Sutherland G.R., Jenkins N.A., Herzog H.;  
 RT "Molecular cloning and characterisation of GPR74 a novel G-protein  
 RT coupled receptor closest related to the Y-receptor family.";  
 RL Brain Res. Mol. Brain Res. 77:199-208(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Liu Q., Guan X.-M., McDonald T.P., Jiang Q., Zeng Z., Marlene J.,  
 RA Williams D.L. Jr., Hong Y., Figueroa D., Clements M.K., Mallee J.,  
 RA Wang R., Evans J., Gould R., Austin C.P.;  
 RT "Identification and characterization of two cognate receptors for  
 RT mammalian FMRFamide-like neuropeptides.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RA Laemmle B.S., Schindler M., Beilmann M., Hamilton B.S., Doods H.N.,  
 RA Wieland H.A.;  
 RT "Cloning and characterization of the NPGP receptor and identification  
 RT of a novel short mRNA isoform in human hypothalamus.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for NPAF (A-18-F-amide) and NPFF (F-8-F-amide)  
 CC neuropeptides, also known as morphine-modulating peptides. Can  
 CC also be activated by a variety of naturally occurring or synthetic  
 CC FMRF-amide like ligands. This receptor mediates its action by  
 CC association with G proteins that activate a phosphatidylinositol-  
 CC calcium second messenger system.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Comment=Experimental confirmation may be lacking for some  
 CC isoforms;  
 CC Name=1; Synonyms=long form;  
 CC IsoId=Q9Y5X5-1; Sequence=Displayed;  
 CC Name=2; Synonyms=short form;  
 CC IsoId=Q9Y5X5-2; Sequence=VSP\_001907;  
 CC Name=3;  
 CC IsoId=Q9Y5X5-3; Sequence=VSP\_001908, VSP\_001909;  
 CC Name=4;  
 CC IsoId=Q9Y5X5-4; Sequence=VSP\_001910, VSP\_001911;  
 CC -!- TISSUE SPECIFICITY: Isoform 1 is abundant in placenta. Relatively  
 CC highly expressed in thymus, testis, and small intestine. Expressed  
 CC at low levels in several tissues including spleen, prostate,  
 CC brain, heart, ovary, colon, kidney, lung, liver and pancreas and  
 CC not expressed in skeletal muscle and leukocytes. Highest but  
 CC relatively low level of isoform 2 in placenta and very low level  
 CC in numerous tissues including adipose tissue and many brain  
 CC regions. Isoform 3 is expressed in brain and heart and, at lower  
 CC levels, in kidney, liver, lung and pancreas.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC HIGHEST TO OREXIN, NPY AND CHOLECYSTOKININ RECEPTORS.  
 CC -!- CAUTION: Ref.4 sequence differs from that shown due to a  
 CC frameshift in position 503.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; AF119815; AAD22047.1; -.  
DR EMBL; AF257210; AAF87078.1; -.  
DR EMBL; AF268899; AAG41398.1; -.  
DR EMBL; AF236083; AAK58513.1; ALT\_FRAME.  
DR EMBL; AF330053; AAK94197.1; -.  
DR EMBL; AJ311393; CAC85427.1; -.  
DR Genew; HGNC:4525; GPR74.  
DR MIM; 607449; -.  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
DR GO; GO:0009582; P:perception of abiotic stimulus; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR005395; NPFF\_receptor.  
DR InterPro; IPR005397; NPFF\_receptor2.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PRINTS; PR01570; NPFFRECEPTOR.  
DR PRINTS; PR01572; NPFFRECEPTR2.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Alternative splicing.

FT	DOMAIN	1	147	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	148	168	1 (POTENTIAL).
FT	DOMAIN	169	184	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	185	205	2 (POTENTIAL).
FT	DOMAIN	206	221	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	222	242	3 (POTENTIAL).
FT	DOMAIN	243	262	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	263	283	4 (POTENTIAL).
FT	DOMAIN	284	319	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	320	340	5 (POTENTIAL).
FT	DOMAIN	341	377	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	378	398	6 (POTENTIAL).
FT	DOMAIN	399	413	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	414	434	7 (POTENTIAL).
FT	DOMAIN	435	522	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	220	308	BY SIMILARITY.
FT	CARBOHYD	110	110	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	122	122	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	300	300	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSP LIC	1	102	Missing (in isoform 2).
FT				/FTId=VSP_001907.
FT	VARSP LIC	1	99	Missing (in isoform 3).
FT				/FTId=VSP_001908.
FT	VARSP LIC	100	100	R -> M (in isoform 3).
FT				/FTId=VSP_001909.
FT	VARSP LIC	101	132	FIMNEKWDTNSSSENWHPIWNVNDTKHHLYSDI -> MAIWK
FT				HDVQDQWIGPGNICRSFSLYVSCNCCR (in isoform
FT				4).
FT				/FTId=VSP_001910.
FT	VARSP LIC	133	522	Missing (in isoform 4).
FT				/FTId=VSP_001911.
FT	CONFLICT	466	466	A -> T (IN REF. 1 AND 4).
SQ	SEQUENCE	522 AA;	60270 MW;	40CB9FCD42F77041 CRC64;

Query Match 100.0%; Score 2208; DB 1; Length 522;  
Best Local Similarity 100.0%; Pred. No. 1.1e-136;  
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEKWDTNSSSENWHPIWNVNDTKHHLYSDINITYVNYLHQPQVAAIFIISYFLIFFLCM 60  
|||||

Db 103 MNEKWDTNSSSENWHPIWNVNDTKHHLYSDINITYVNYYLHQPQVAAIFIISYFLIFFLCM 162

Qy 61 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIAGWPGNTMCKI 120  
 |||

Db 163 MGNTVVCFIVMRNKHMTVTNLFILNLAISDLLVGIFCMPITLLDNIAGWPGNTMCKI 222

Qy 121 SGLVQGISVAASVFTLVAVDRFQCVVYPFKPKLTIKTAFVIIMI IWVLAITIMSPSAV 180  
 |||

Db 223 SGLVQGISVAASVFTLVAVDRFQCVVYPFKPKLTIKTAFVIIMI IWVLAITIMSPSAV 282

Qy 181 MLHVQEEKYYRVRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANIY LAPLSLIVIMYG 240  
 |||

Db 283 MLHVQEEKYYRVRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANIY LAPLSLIVIMYG 342

Qy 241 RIGISLFRAAVPHTGRKNQE QWHVSRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 300  
 |||

Db 343 RIGISLFRAAVPHTGRKNQE QWHVSRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYA 402

Qy 301 DLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKPM 360  
 |||

Db 403 DLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKPM 462

Qy 361 EAYALKAKSHVLINTSNQLVQESTFQNP HGETLLYRKSAEKPQQLVMEELKETTSNSEI 420  
 |||

Db 463 EAYALKAKSHVLINTSNQLVQESTFQNP HGETLLYRKSAEKPQQLVMEELKETTSNSEI 522

Result No.	Score	Query Match	Length	DB	ID	Description
1	1748.5	79.2	417	11	Q924H0	Q924h0 mus musculu
2	1748.5	79.2	417	11	Q8BKR6	Q8bkr6 mus musculu
3	1666	75.5	405	11	Q924N0	Q924n0 mus musculu
4	984	44.6	432	11	Q924G9	Q924g9 rattus norv
5	553	25.0	758	5	Q7YU49	Q7yu49 drosophila
6	499.5	22.6	425	4	Q9HBV6	Q9hbv6 homo sapien
7	487.5	22.1	449	5	Q9VB87	Q9vb87 drosophila
8	487	22.1	422	11	Q8VHD7	Q8vhd7 rattus norv
9	486.5	22.0	365	11	Q8BHH0	Q8bhh0 mus musculu
10	485	22.0	600	5	Q9VW75	Q9vw75 drosophila
11	476	21.6	402	5	Q964E5	Q964e5 dugesia tig
12	470.5	21.3	429	5	P92045	P92045 lymnaea sta
13	469.5	21.3	364	11	Q8BV78	Q8bv78 mus musculu
14	463.5	21.0	381	11	Q8BWV1	Q8bwv1 mus musculu
15	460.5	20.9	381	11	Q9ERC0	Q9erc0 rattus norv
16	455.5	20.6	540	5	Q9VRM0	Q9vrm0 drosophila
17	451.5	20.4	375	13	O57463	O57463 brachydanio